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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=2; day=23; hr=13; min=57; sec=11; ms=939; ]

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Reviewer Comments:

1.

E355 Empty lines found between the amino acid numbering and the proteins SEQID ( 2 )

E321 No. of Bases conflict, this line has no nucleotides  
SEQID (2) POS (256)

<210> 2

<211> 498

<212> PRT

<213> Saccharomyces cerevisiae

<220>

<223> DNA

\* \* \* \* \*

Gly	Val	His	Trp	Asn	Phe	Phe	Ile	Thr	Leu	Ser	Leu	Leu	Pro	Leu	Val
				245					250					255	

Leu	Thr	Phe	Ile	Asp	Pro	Val	Thr	Arg	Met	Val	Pro	Arg	Cys	Ser	Ile
				260					265					270	

Ala	Ile	Phe	Ile	Ser	Cys	Ile	Tyr	Glu	Trp	Leu	Leu	Leu	Lys	Asp	Asp
				275					280					285	

Arg	Thr	Leu	Asn	Phe	Leu	Ile	Leu	Ala	Asp	Arg	Asn	Cys	Phe	Phe	Ser
				290				295						300	

For SEQ ID # 2, the sequence rules specify the numbering for amino acids

be placed below the line of amino acids in a protein or coding region of a nucleotide sequence.

"Sec. 1.822 Symbols and format to be used for nucleotide and/or amino acid sequence data.

(a) The symbols and format to be used for nucleotide and/or amino acid sequence data shall conform to the requirements of paragraphs (b) through (e) of this section.

(d) Representation of amino acids. (1) The amino acids in a protein or peptide sequence shall be listed using the three-letter abbreviation with the first letter as an upper case character, as in WIPO Standard ST.25 (1998), Appendix 2, Table 3.

(4) The enumeration of amino acids may start at the first amino acid of the first mature protein, with the number 1. When presented, the amino acids preceding the mature protein, e.g., pre-sequences, pro-sequences, pre-pro-sequences and signal sequences, shall have negative numbers, counting backwards starting with the amino acid next to number 1. Otherwise, the enumeration of amino acids shall start at the first amino acid at the amino terminal as number 1. It shall be marked below the sequence every 5 amino acids."

In the SEQ ID # 2 there are blank lines found between the amino acids with the numbers 260 through 270. Please remove any and all blank lines found between the amino acids and the numbering in these sequences.

2.

E355 Empty lines found between the amino acid numbering and the proteins SEQID ( 13 )

E321 No. of Bases conflict, this line has no nucleotides  
SEQID (13) POS (208)

E300 Invalid codon found Arg SEQID (13) POS: 625

E300 Invalid codon found Ala SEQID (13) POS: 628

E300 Invalid codon found Thr SEQID (13) POS: 631

E300 Invalid codon found Lys SEQID (13) POS: 634

E300 Invalid codon found Ala SEQID (13) POS: 637

E300 Invalid codon found Gln SEQID (13) POS: 640

E300 Invalid codon found Trp SEQID (13) POS: 643

E300 Invalid codon found Val SEQID (13) POS: 646

E300 Invalid codon found Lys SEQID (13) POS: 649

E300 Invalid codon found Glu SEQID (13) POS: 652

E300 Invalid codon found Lys SEQID (13) POS: 655

E300 Invalid codon found Gly SEQID (13) POS: 658

E300 Invalid codon found Arg SEQID (13) POS: 661

E300 Invalid codon found Leu SEQID (13) POS: 664

E300 Invalid codon found Pro SEQID (13) POS: 667  
E300 Invalid codon found Phe SEQID (13) POS: 670

<210> 13

<211> 1797

<212> DNA

<213> Cryptococcus neoformans

<220>

<221> CDS

<222> (1)..(1794)

\* \* \* \* \*

agg	tcg	cta	tta	gaa	gga	gtt	tcg	ctt	gat	gtt	ccg	tca	cat	atc	gac	576
Arg	Ser	Leu	Leu	Glu	Gly	Val	Ser	Leu	Asp	Val	Pro	Ser	His	Ile	Asp	
			180					185					190			

tcc	aag	gtc	aga	ata	tct	cct	gtt	ccc	tac	ttg	agg	ctc	aaa	aag	tct	624
Ser	Lys	Val	Arg	Ile	Ser	Pro	Val	Pro	Tyr	Leu	Arg	Leu	Lys	Lys	Ser	
		195					200					205				

agg	gca	acg	aag	gcg	caa	tgg	gtg	aaa	gaa	aag	gga	aga	tta	cca	ttt	672
Arg	Ala	Thr	Lys	Ala	Gln	Trp	Val	Lys	Glu	Lys	Gly	Arg	Leu	Pro	Phe	
	210					215						220				

ttg	aca	gtg	tac	cga	gcg	cac	atg	atg	ctc	atg	act	gtt	atc	tgc	atc	720
Leu	Thr	Val	Tyr	Arg	Ala	His	Met	Met	Leu	Met	Thr	Val	Ile	Cys	Ile	
225						230				235				240		

A.

SEQ ID # 13 has the same problem as SEQ ID # 2 for amino acids numbered 210 through 220. Please remove any and all blank lines between the amino acids and the numbering in this region.

B. The sequence rules specify the amino acids in the coding region of a sequence be entered "immediately" below the codons.

"Sec. 1.822 Symbols and format to be used for nucleotide and/or amino acid sequence data.

(c) Format representation of nucleotides. (1) A nucleotide sequence shall be listed using the lower-case letter for representing the one-letter code for the nucleotide bases set forth in WIPO Standard ST.25 (1998), Appendix 2, Table 1.

3) The bases in the coding parts of a nucleotide sequence shall be listed as triplets (codons). The amino acids corresponding to the codons in the coding parts of a nucleotide sequence shall be typed immediately below the corresponding codons. Where a codon spans an intron, the amino acid symbol shall be typed below the portion of the codon containing two nucleotides.

There are blank lines between the codons and amino acids for nucleotides 577 through 624. Please remove any and all blank lines found in this region of the sequence.

3.

W402	Undefined organism found in <213> in SEQ ID (12)
W402	Undefined organism found in <213> in SEQ ID (13)
W402	Undefined organism found in <213> in SEQ ID (14)
W213	Artificial or Unknown found in <213> in SEQ ID (15)
W213	Artificial or Unknown found in <213> in SEQ ID (16)

The warnings shown above are ok and require no response.

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**Input Set:**

**Output Set:**

**Started:** 2010-02-08 15:57:27.638  
**Finished:** 2010-02-08 15:57:33.049  
**Elapsed:** 0 hr(s) 0 min(s) 5 sec(s) 411 ms  
**Total Warnings:** 5  
**Total Errors:** 36  
**No. of SeqIDs Defined:** 18  
**Actual SeqID Count:** 18

Error code	Error Description
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (13)
E 300	Invalid codon found Arg SEQID (13) POS: 625
E 300	Invalid codon found Ala SEQID (13) POS: 628
E 300	Invalid codon found Thr SEQID (13) POS: 631
E 300	Invalid codon found Lys SEQID (13) POS: 634
E 300	Invalid codon found Ala SEQID (13) POS: 637
E 300	Invalid codon found Gln SEQID (13) POS: 640
E 300	Invalid codon found Trp SEQID (13) POS: 643
E 300	Invalid codon found Val SEQID (13) POS: 646
E 300	Invalid codon found Lys SEQID (13) POS: 649
E 300	Invalid codon found Glu SEQID (13) POS: 652
E 300	Invalid codon found Lys SEQID (13) POS: 655
E 300	Invalid codon found Gly SEQID (13) POS: 658
E 300	Invalid codon found Arg SEQID (13) POS: 661
E 300	Invalid codon found Leu SEQID (13) POS: 664
E 300	Invalid codon found Pro SEQID (13) POS: 667
E 300	Invalid codon found Phe SEQID (13) POS: 670
W 402	Undefined organism found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)



# SEQUENCE LISTING

<110> Tsukahara, Kappei  
 Tsuchiya, Mamiko  
 Jigami, Yoshifumi  
 Nakayama, Kenichi  
 Umemura, Mariko  
 Okamoto, Michiyo

<120> METHOD OF SCREENING FOR COMPOUNDS THAT  
 INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT

<130> 082368-004400US

<140> 10536935

<141> 2006-02-15

<150> PCT/JP03/14909

<151> 2003-11-21

<150> JP 2002-339418

<151> 2002-11-22

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1497

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1494)

<400> 1

atg gca aca gta cat cag aag aat atg tcg act tta aaa cag aga aaa	48
Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys	
1 5 10 15	

gag gac ttt gtg aca ggg ctc aat ggc ggt tct ata aca gaa att aac	96
Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn	
20 25 30	

gca gtg aca tca att gct ttg gta act tac ata tca tgg aac tta ttg	144
Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu	
35 40 45	

aaa aat tcc aac ctt atg cct cct ggc att tcc agc gtg caa tac ata	192
Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile	
50 55 60	

att gat ttt gca ttg aac tgg gtt gct ttg ctt cta tct att act att	240
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Ile	Asp	Phe	Ala	Leu	Asn	Trp	Val	Ala	Leu	Leu	Leu	Ser	Ile	Thr	Ile	288
65					70					75					80	
tat	gct	agt	gaa	cca	tac	ctt	cta	aac	acg	cta	ata	ctg	tta	cct	tgt	
Tyr	Ala	Ser	Glu	Pro	Tyr	Leu	Leu	Asn	Thr	Leu	Ile	Leu	Leu	Pro	Cys	
				85					90					95		
ttg	ctc	gca	ttc	ata	tat	gga	aaa	ttt	act	agc	tcg	agt	aaa	cct	tct	336
Leu	Leu	Ala	Phe	Ile	Tyr	Gly	Lys	Phe	Thr	Ser	Ser	Ser	Lys	Pro	Ser	
			100					105					110			
aat	cca	ata	tac	aat	aaa	aaa	aaa	atg	att	aca	cag	cgg	ttc	caa	cta	384
Asn	Pro	Ile	Tyr	Asn	Lys	Lys	Lys	Met	Ile	Thr	Gln	Arg	Phe	Gln	Leu	
		115					120					125				
gaa	aaa	aag	ccg	tat	att	act	gcg	tat	cgt	ggg	ggg	atg	ctt	att	ctg	432
Glu	Lys	Lys	Pro	Tyr	Ile	Thr	Ala	Tyr	Arg	Gly	Gly	Met	Leu	Ile	Leu	
	130					135				140						
act	gct	att	gcc	atc	ttg	gct	gta	gat	ttt	cca	att	ttc	cca	agg	agg	480
Thr	Ala	Ile	Ala	Ile	Leu	Ala	Val	Asp	Phe	Pro	Ile	Phe	Pro	Arg	Arg	
145					150					155					160	
ttt	gcc	aag	gtg	gaa	act	tgg	ggg	aca	tcc	ctg	atg	gat	ctt	ggg	gta	528
Phe	Ala	Lys	Val	Glu	Thr	Trp	Gly	Thr	Ser	Leu	Met	Asp	Leu	Gly	Val	
			165					170					175			
gga	tca	ttc	gtt	ttc	agt	aac	ggg	att	gtt	tct	tct	agg	gca	ctg	ttg	576
Gly	Ser	Phe	Val	Phe	Ser	Asn	Gly	Ile	Val	Ser	Ser	Arg	Ala	Leu	Leu	
			180					185					190			
aaa	aac	cta	agc	ttg	aag	agt	aaa	ccc	agc	ttc	tta	aaa	aat	gca	ttt	624
Lys	Asn	Leu	Ser	Leu	Lys	Ser	Lys	Pro	Ser	Phe	Leu	Lys	Asn	Ala	Phe	
		195					200					205				
aat	gcc	tta	aaa	tca	gga	gga	act	cta	ttg	ttc	cta	gga	ttg	ctg	agg	672
Asn	Ala	Leu	Lys	Ser	Gly	Gly	Thr	Leu	Leu	Phe	Leu	Gly	Leu	Leu	Arg	
	210					215					220					
ttg	ttt	ttt	gta	aaa	aat	ttg	gaa	tat	caa	gaa	cat	gtc	aca	gaa	tat	720
Leu	Phe	Phe	Val	Lys	Asn	Leu	Glu	Tyr	Gln	Glu	His	Val	Thr	Glu	Tyr	
225					230					235					240	
ggg	gtt	cat	tgg	aat	ttt	ttt	atc	acc	cta	tca	ttg	ttg	cca	ctt	gta	768
Gly	Val	His	Trp	Asn	Phe	Phe	Ile	Thr	Leu	Ser	Leu	Leu	Pro	Leu	Val	
			245						250					255		
ttg	acc	ttt	att	gat	ccc	gtc	aca	aga	atg	gtt	cca	cgc	tgc	tca	att	816
Leu	Thr	Phe	Ile	Asp	Pro	Val	Thr	Arg	Met	Val	Pro	Arg	Cys	Ser	Ile	
			260					265					270			
gca	ata	ttc	att	tca	tgc	att	tat	gaa	tgg	cta	ctt	tta	aag	gac	gat	864
Ala	Ile	Phe	Ile	Ser	Cys	Ile	Tyr	Glu	Trp	Leu	Leu	Leu	Lys	Asp	Asp	
		275														

290	295	300	
gct aat aga gaa ggc atc ttc tca ttt cta ggt tat tgc tcg att ttt			960
Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe			
305	310	315	320
ctt tgg ggc caa aac acg gga ttt tac ttg ttg gga aat aaa cca act			1008
Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr			
	325	330	335
tta aac aat ctt tat aag cct tct acg caa gac gta gtt gca gca tca			1056
Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser			
	340	345	350
aag aag tct tcg act tgg gac tat tgg act tca gta acc cca tta agt			1104
Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser			
	355	360	365
ggc ctc tgt ata tgg agt aca att ttt ctt gtt atc agc cag ttg gtt			1152
Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val			
	370	375	380
ttt caa tac cat cct tat agt gtt tca aga agg ttt gct aac tta cca			1200
Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro			
385	390	395	400
tat act ttg tgg gtc att act tat aat tta cta ttt ttg act ggg tac			1248
Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr			
	405	410	415
tgc ttg act gac aaa att ttc ggt aat tct tcg gaa tat tat aaa gtt			1296
Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val			
	420	425	430
gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg			1344
Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu			
	435	440	445
ttg gca aat gtc tct act ggt tta gtc aat atg tct atg gtc acg ata			1392
Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile			
	450	455	460
gat tct tca ccc tta aaa tca ttc ctg gtt ttg ttg gca tac tgc tca			1440
Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser			
465	470	475	480
ttc ata gct gtc ata tcg gtt ttc ttg tat aga aaa aga ata ttc att			1488
Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile			
	485	490	495
aag cta taa			1497
Lys Leu			

<210> 2

<211> 498

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<223> DNA

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Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys  
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Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn  
20 25 30

Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu  
35 40 45

Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile  
50 55 60

Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile  
65 70 75 80

Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys  
85 90 95

Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser  
100 105 110

Asn Pro Ile Tyr Asn Lys Lys Lys Met Ile Thr Gln Arg Phe Gln Leu  
115 120 125

Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu  
130 135 140

Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg  
145 150 155 160

Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val  
165 170 175

Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu  
180 185 190

Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe  
195 200 205

Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg  
210 215 220

Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr  
225 230 235 240

Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val  
245 250 255

Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile

260	265	270
Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Leu Lys Asp Asp		
275	280	285
Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser		
290	295	300
Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe		
305	310	315
Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr		
	325	330
Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser		
	340	345
Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser		
	355	360
Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val		
	370	375
Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro		
385	390	395
Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr		
	405	410
Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val		
	420	425
Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu		
	435	440
Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile		
	450	455
Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser		
465	470	475
Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile		
	485	490
		495
Lys Leu		

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 <212> DNA  
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 <220>  
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 <222> (1)..(1455)

<400> 3

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Met Ser Ser Ser Leu Lys Gln Leu Lys Glu Gln Phe Val Ser Asp Leu	
1 5 10 15	
act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta	96
Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu	
20 25 30	
tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta	144
Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu	
35 40 45	
gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc	192
Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser	
50 55 60	
att act gtt tat agc aac agc cct tct tat ttg cat tat ttt att gtt	240
Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val	
65 70 75 80	
att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca	288
Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro	
85 90 95	
tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa	336
Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu	
100 105 110	
cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg	384
Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu	
115 120 125	
ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca	432
Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro	
130 135 140	
aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta	480
Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu	
145 150 155 160	
gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa	528
Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln	
165 170 175	
ttg atc aag aac cac acc gac aac tac aaa ttt agt tgg aag agt tat	576
Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr	
180 185 190	
ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt	624
Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val	
195 200 205	
tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa	672
Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu	
210 215 220	

cac	gaa	aca	gag	tat	gga	atc	cat	tgg	aat	ttt	ttc	ttc	aca	tta	ggg	720
His	Glu	Thr	Glu	Tyr	Gly	Ile	His	Trp	Asn	Phe	Phe	Phe	Thr	Leu	Gly	
225					230					235					240	
ttc	ttg	cca	att	gta	ttg	gga	ata	tta	gac	ccg	gtg	ttg	aat	ttg	gtt	768
Phe	Leu	Pro	Ile	Val	Leu	Gly	Ile	Leu	Asp	Pro	Val	Leu	Asn	Leu	Val	
				245					250					255		
cca	cgc	ttc	ata	ata	gga	att	ggg	atc	tca	att	gct	tat	gag	gta	gcg	816
Pro	Arg	Phe	Ile	Ile	Gly	Ile	Gly	Ile	Ser	Ile	Ala	Tyr	Glu	Val	Ala	
			260					265					270			
ttg	aat	aag	act	ggg	ttg	ttg	aag	ttc	att	ttg	agc	agc	gaa	aac	aga	864
Leu	Asn	Lys	Thr	Gly	Leu	Leu	Lys	Phe	Ile	Leu	Ser	Ser	Glu	Asn	Arg	
		275					280					285				
ctt	gaa	tct	ctc	atc	acc	atg	aat	aaa	gaa	ggg	att	ttt	tcg	ttt	att	912
Leu	Glu	Ser	Leu	Ile	Thr	Met	Asn	Lys	Glu	Gly	Ile	Phe	Ser	Phe	Ile	
	290					295					300					
gga	tat	ctt	tgt	att	ttt	ata	att	ggg	cag	tct	ttt	ggg	tca	ttt	gtt	960
Gly	Tyr	Leu	Cys	Ile	Phe	Ile	Ile	Gly	Gln	Ser	Phe	Gly	Ser	Phe	Val	
305					310					315					320	
tta	aca	ggc	tac	aaa	aca	aag	aac	aac	tta	ata	acc	att	agc	aaa	att	1008
Leu	Thr	Gly	Tyr	Lys	Thr	Lys	Asn	Asn	Leu	Ile	Thr	Ile	Ser	Lys	Ile	
				325					330					335		
cgt	att	tca	aaa	aaa	caa	cac	aag	aaa	gag	ctg	ctg	ctg	ttt	ttc	tca	1056
Arg	Ile	Ser	Lys	Lys	Gln	His	Lys	Lys	Glu	Leu	Leu	Leu	Phe	Phe	Ser	
			340					345					350			
gtc	gcc	act	act	cag	gga	tta	tat	ttg	gca	tgt	atc	ttc	tat	cac	tta	1104
Val	Ala	Thr	Thr	Gln	Gly	Leu	Tyr	Leu	Ala	Cys	Ile	Phe	Tyr	His	Leu	
		355					360					365				
gct	ttc	agt	ttg	ttc	atc	agc	aac	tta	tca	ttc	ttg	caa	cca	att	tca	1152
Ala	Phe	Ser	Leu	Phe	Ile	Ser	Asn	Leu	Ser	Phe	Leu	Gln	Pro	Ile	Ser	
	370					375					380					
aga	cga	ttg	gcc	aat	ttc	ccc	tac	gtc	atg	tgg	gtc	gtt	tcg	tac	aat	1200
Arg	Arg	Leu	Ala	Asn	Phe	Pro	Tyr	Val	Met	Trp	Val	Val	Ser	Tyr	Asn	
385					390					395					400	
gct	acg	ttt	tta	tta	tgt	tat	gac	tta	att	gaa	aaa	ttt	atc	ccg	ggg	1248
Ala	Thr	Phe	Leu	Leu	Cys	Tyr	Asp	Leu	Ile	Glu	Lys	Phe	Ile	Pro	Gly	
				405					410					415		
aac	ctt	act	tct	act	gta	ttg	gac	tct	att	aat	aac	aat	ggg	tta	ttt	1296
Asn	Leu	Thr	Ser	Thr	Val	Leu	Asp	Ser	Ile	Asn	Asn	Asn	Gly	Leu	Phe	
			420					425					430			
atc	ttc	ttg	gtc	agc	aat	tta	tta	aca	ggg	ttt						

aac act ttg gaa act agc aat aaa atg gca gtg att atc ttg att ggc 1392  
 Asn Thr Leu Glu Thr Ser Asn Lys Met Ala Val Ile Ile Leu Ile Gly  
 450 455 460

tat agt ctt act tgg aca ttg ctc gcc tta tat ttg gat aag agg aag 1440  
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atc tac atc aag ctt tag 1458  
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Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu  
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Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Lys Ser Leu Gly Asp Leu  
 35 40 45

Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser  
 50 55 60

Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val  
 65 70 75 80

Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro  
 85 90 95

Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu  
 100 105 110

Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu  
 115 120 125

Ile Il